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# 3

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## RAW SEQUENCE LISTING

DATE: 10/24/2002

PATENT APPLICATION: US/09/978,418

TIME: 14:51:34

Input Set : A:\SEQLIST-9Oct2002.txt

Output Set: N:\CRF4\10242002\I978418.raw

3 <110> APPLICANT: Bejanin, Stephan  
 4 Tanaka, Hiroaki  
 6 <120> TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF  
 8 <130> FILE REFERENCE: 142.US5.REG  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/978,418  
 C--> 11 <141> CURRENT FILING DATE: 2002-10-15  
 13 <150> PRIOR APPLICATION NUMBER: 60/311,305  
 14 <151> PRIOR FILING DATE: 2001-08-10  
 17 <150> PRIOR APPLICATION NUMBER: 60/314,734  
 18 <151> PRIOR FILING DATE: 2001-08-24  
 20 <150> PRIOR APPLICATION NUMBER: 60/318,204  
 21 <151> PRIOR FILING DATE: 2001-09-07  
 23 <150> PRIOR APPLICATION NUMBER: 60/326,470  
 24 <151> PRIOR FILING DATE: 2001-10-01  
 26 <160> NUMBER OF SEQ ID NOS: 52  
 28 <170> SOFTWARE: JPatent  
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 31 <211> LENGTH: 850  
 32 <212> TYPE: DNA  
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 58 tgtgtgggcg tgggggcagt ctgcccagg ctggtctgga actcctggcc tcaagtgatc 180  
 59 ctctctcgtc aagatatgaa caggagtaca gctgtgtagt aaag atg cct tct ggt 236  
 60 Met Pro Ser Gly  
 61 1  
 62 gaa ttt gca cgt ata tgc cga gat ctc agc cat att gga gat gct gtt 284

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63 Glu Phe Ala Arg Ile Cys Arg Asp Leu Ser His Ile Gly Asp Ala Val
64 5 10 15 20
65 gta att tcc tgt gca aaa gac gga gtg aaa ttt tct gca agt gga gaa 332
66 Val Ile Ser Cys Ala Lys Asp Gly Val Lys Phe Ser Ala Ser Gly Glu
67 25 30 35
68 ctt gga aat gga aac att aaa ttg tca cag aca agt aat gtc gat aaa 380
69 Leu Gly Asn Gly Asn Ile Lys Leu Ser Gln Thr Ser Asn Val Asp Lys
70 40 45 50
71 gag gag gaa gct gtt acc ata gag atg aat gaa cca gtt caa cta act 428
72 Glu Glu Glu Ala Val Thr Ile Glu Met Asn Glu Pro Val Gln Leu Thr
73 55 60 65
74 ttt gca ctg agg tac ctg aac ttc ttt aca aaa gcc act cca ctc tct 476
75 Phe Ala Leu Arg Tyr Leu Asn Phe Phe Thr Lys Ala Thr Pro Leu Ser
76 70 75 80
77 tca acg gtg aca ctc agt atg tct gca gat gta ccc ctt gtt gta gag 524
78 Ser Thr Val Thr Leu Ser Met Ser Ala Asp Val Pro Leu Val Val Glu
79 85 90 95 100
80 tat aaa att gcg gat atg gga cac tta aaa tac tac ttg gct ccc aag 572
81 Tyr Lys Ile Ala Asp Met Gly His Leu Lys Tyr Tyr Leu Ala Pro Lys
82 105 110 115
83 atc gag gat gaa gaa gga tct taggcattct taaaattcaa gaaaataaaa 623
84 Ile Glu Asp Glu Glu Gly Ser
85 120
86 ctaagctctt tgagaactgc ttctaagatg ccagcatata ctgaagtctt ttctgtcacc 683
87 aaatttgtac ctctaagtac atatgtatg attgttttct gtaaataacc tatttttttc 743
88 tctattctct gcaatttggt taaagaataa agtccaaagt cagatctggg ctagttaaaa 803
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92 <211> LENGTH: 123
93 <212> TYPE: PRT
94 <213> ORGANISM: Homo sapiens
96 <400> SEQUENCE: 2
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98 1 5 10 15
99 Gly Asp Ala Val Val Ile Ser Cys Ala Lys Asp Gly Val Lys Phe Ser
100 20 25 30
101 Ala Ser Gly Glu Leu Gly Asn Gly Asn Ile Lys Leu Ser Gln Thr Ser
102 35 40 45
103 Asn Val Asp Lys Glu Glu Glu Ala Val Thr Ile Glu Met Asn Glu Pro
104 50 55 60
105 Val Gln Leu Thr Phe Ala Leu Arg Tyr Leu Asn Phe Phe Thr Lys Ala
106 65 70 75 80
107 Thr Pro Leu Ser Ser Thr Val Thr Leu Ser Met Ser Ala Asp Val Pro
108 85 90 95
109 Leu Val Val Glu Tyr Lys Ile Ala Asp Met Gly His Leu Lys Tyr Tyr
110 100 105 110
111 Leu Ala Pro Lys Ile Glu Asp Glu Glu Gly Ser
112 115 120
114 <210> SEQ ID NO: 3

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125 <222> LOCATION: 91..777
127 <220> FEATURE:
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129 <222> LOCATION: 778..883
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132 <221> NAME/KEY: polyA_signal
133 <222> LOCATION: 826..831
135 <220> FEATURE:
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137 <222> LOCATION: 848..883
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141 tctgagctca gttgcagtac tcgggaagcc atg cag gat gaa gat gga tac atc 114
142 Met Gln Asp Glu Asp Gly Tyr Ile
143 1 5
144 acc tta aat att aaa act cgg aaa cca gct ctc gtc tcc gtt ggc tct 162
145 Thr Leu Asn Ile Lys Thr Arg Lys Pro Ala Leu Val Ser Val Gly Ser
146 10 15 20
147 gca tcc tcc tcc tgg tgg cgt gtg atg gct ttg att ctg ctg atc ctg 210
148 Ala Ser Ser Ser Trp Trp Arg Val Met Ala Leu Ile Leu Leu Ile Leu
149 25 30 35 40
150 tgc gtg ggg atg gtt gtc ggg ctg gtg gct ctg ggg att tgg tct gtc 258
151 Cys Val Gly Met Val Val Gly Leu Val Ala Leu Gly Ile Trp Ser Val
152 45 50 55
153 atg cag cgc aat tac cta caa gat gag aat gaa aat cgc aca gga act 306
154 Met Gln Arg Asn Tyr Leu Gln Asp Glu Asn Glu Asn Arg Thr Gly Thr
155 60 65 70
156 ctg caa caa tta gca aag cgc ttc tgt caa tat gtg gta aaa caa tca 354
157 Leu Gln Gln Leu Ala Lys Arg Phe Cys Gln Tyr Val Val Lys Gln Ser
158 75 80 85
159 gaa cta aag ggc act ttc aaa ggt cat aaa tgc agc ccc tgt gac aca 402
160 Glu Leu Lys Gly Thr Phe Lys Gly His Lys Cys Ser Pro Cys Asp Thr
161 90 95 100
162 aac tgg aga tat tat gga gat agc tgc tat ggg ttc ttc agg cac aac 450
163 Asn Trp Arg Tyr Tyr Gly Asp Ser Cys Tyr Gly Phe Phe Arg His Asn
164 105 110 115 120
165 tta aca tgg gaa gag agt aag cag tac tgc act gac atg aat gct act 498
166 Leu Thr Trp Glu Glu Ser Lys Gln Tyr Cys Thr Asp Met Asn Ala Thr
167 125 130 135
168 ctc ctg aag att gac aac cgg aac att gtg gag tac atc aaa gcc agg 546
169 Leu Leu Lys Ile Asp Asn Arg Asn Ile Val Glu Tyr Ile Lys Ala Arg

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170          140          145          150
171 act cat tta att cgt tgg gtc gga tta tct cgc cag aag tcg aat gag 594
172 Thr His Leu Ile Arg Trp Val Gly Leu Ser Arg Gln Lys Ser Asn Glu
173          155          160          165
174 gtc tgg aag tgg gag gat ggc tcg gtt atc tca gaa aat atg ttt gag 642
175 Val Trp Lys Trp Glu Asp Gly Ser Val Ile Ser Glu Asn Met Phe Glu
176          170          175          180
177 ttt ttg gaa gat gga aaa gga aat atg aat tgt gct tat ttt cat aat 690
178 Phe Leu Glu Asp Gly Lys Gly Asn Met Asn Cys Ala Tyr Phe His Asn
179 185          190          195          200
180 ggg aaa atg cac cct acc ttc tgt gag aac aaa cat tat tta atg tgt 738
181 Gly Lys Met His Pro Thr Phe Cys Glu Asn Lys His Tyr Leu Met Cys
182          205          210          215
183 gag agg aag gct ggc atg acc aag gtg gac caa cta cct taatgcaaag 787
184 Glu Arg Lys Ala Gly Met Thr Lys Val Asp Gln Leu Pro
185          220          225
186 aggtggacag gataacacag ataagggctt tattgtacaa taaaagatat gtatgaatgc 847
187 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 883
189 <210> SEQ ID NO: 4
190 <211> LENGTH: 229
191 <212> TYPE: PRT
192 <213> ORGANISM: Homo sapiens
194 <400> SEQUENCE: 4
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198          20          25          30
199 Met Ala Leu Ile Leu Leu Ile Leu Cys Val Gly Met Val Val Gly Leu
200          35          40          45
201 Val Ala Leu Gly Ile Trp Ser Val Met Gln Arg Asn Tyr Leu Gln Asp
202          50          55          60
203 Glu Asn Glu Asn Arg Thr Gly Thr Leu Gln Gln Leu Ala Lys Arg Phe
204 65          70          75          80
205 Cys Gln Tyr Val Val Lys Gln Ser Glu Leu Lys Gly Thr Phe Lys Gly
206          85          90          95
207 His Lys Cys Ser Pro Cys Asp Thr Asn Trp Arg Tyr Tyr Gly Asp Ser
208          100          105          110
209 Cys Tyr Gly Phe Phe Arg His Asn Leu Thr Trp Glu Glu Ser Lys Gln
210          115          120          125
211 Tyr Cys Thr Asp Met Asn Ala Thr Leu Leu Lys Ile Asp Asn Arg Asn
212          130          135          140
213 Ile Val Glu Tyr Ile Lys Ala Arg Thr His Leu Ile Arg Trp Val Gly
214 145          150          155          160
215 Leu Ser Arg Gln Lys Ser Asn Glu Val Trp Lys Trp Glu Asp Gly Ser
216          165          170          175
217 Val Ile Ser Glu Asn Met Phe Glu Phe Leu Glu Asp Gly Lys Gly Asn
218          180          185          190
219 Met Asn Cys Ala Tyr Phe His Asn Gly Lys Met His Pro Thr Phe Cys
220          195          200          205

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223 Val Asp Gln Leu Pro
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237 <222> LOCATION: 235..2562
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241 <222> LOCATION: 2563..3230
243 <400> SEQUENCE: 5
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245 ttttggtatc actcctagta ccaagtcttg tgtctgtcaa tatcctgtcc aaaaaagaaa 120
246 aacacaccaa ggaaaattaa tataggaaaa atttaaaaag ttattagagg actgaaaata 180
247 taaaaatgga aactgaaag acacagagtt tttattttca gcactgcagc tctg atg 237
248                                     Met
249                                     1
250 gtc cag ctc cac cag gac aca gat ccc cag atc cct aaa ggt cag cca 285
251 Val Gln Leu His Gln Asp Thr Asp Pro Gln Ile Pro Lys Gly Gln Pro
252      5                      10                      15
253 tgc acc ctg aac agc tca gag gga gga gcc agg cca gca gtg cct cac 333
254 Cys Thr Leu Asn Ser Ser Glu Gly Gly Ala Arg Pro Ala Val Pro His
255      20                      25                      30
256 acc ttg ttc tct tct gct cta gac aga tgg ctc cat aat gac agc ttc 381
257 Thr Leu Phe Ser Ser Ala Leu Asp Arg Trp Leu His Asn Asp Ser Phe
258      35                      40                      45
259 ata atg gca gtg ggt gag ccc ctg gtg cac atc agg gtc act ctt ctg 429
260 Ile Met Ala Val Gly Glu Pro Leu Val His Ile Arg Val Thr Leu Leu
261 50                      55                      60                      65
262 ctg ctc tgg ttt gga atg ttt ttg tct att tct ggc cac tct cag gcc 477
263 Leu Leu Trp Phe Gly Met Phe Leu Ser Ile Ser Gly His Ser Gln Ala
264      70                      75                      80
265 agg ccc tcc cag tat ttc act tct cca gaa gtg gtg atc cct ttg aag 525
266 Arg Pro Ser Gln Tyr Phe Thr Ser Pro Glu Val Val Ile Pro Leu Lys
267      85                      90                      95
268 gtg atc agc agg ggc aga ggt gca aag gct cct gga tgg ctc tcc tat 573
269 Val Ile Ser Arg Gly Arg Gly Ala Lys Ala Pro Gly Trp Leu Ser Tyr
270      100                      105                      110
271 agc ctg cgg ttt ggg gga cag aga tac att gtc cac atg agg gta aat 621
272 Ser Leu Arg Phe Gly Gly Gln Arg Tyr Ile Val His Met Arg Val Asn
273      115                      120                      125
274 aag ctg ttg ttt gct gca cac ctt cct gtg ttc acc tac aca gag cag 669

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## VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date